

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 100248

To: Ulrike Winkler

Location: CM1 8E12

Art Unit: 1648

Wednesday, August 06, 2003

Case Serial Number: 09/303510

From: Beverly Shears

**Location: Biotech-Chem Library** 

CM1-1E05

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## Search Notes

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GITTCTGTGTTCCTCGGGAATGTCACTGAGCTTATACATCTGGGTCTCTGGGAGCTGCAGTG 62 GATGGGCATTTGTGACAGCACTATGGGACTGAGTCACACTCTCCTTGTGATGGCCCTCTG CTCTCTGGTGTTTCTTCCATGAAGAGTCAAGCATATTTCAACAAGACTGGAAGTGCCAT 184 GCCAITTTACAAACTCTCAAAAAATAAGCCTGGATGAGCTGGTAGTATTTGGCAGGACCA GCCATTTTACAAACTCTCAAAACATAAGCCTGGATGAGCTGGTAGTATTTTGGCAGGACCA 62 GATGGGCATTIGTGACACCACTATGGGACTGAGTCACACTCTCCTTGTGATGGCCCTCCTG GATGGGCATTIGIGACAGCACTATGGGACTGAGACTCTCCTTGTGATGGCCCTCCTG 184 GCCATTTTACAAACTCTCAAAACATAAGCCTGGATGAGCTGGTAGTATTTTGGCAGGACCA GENALIGN - Multiple Sequence Alignment Program Release 5.4 Region Alignment: (listed in Clustered order) Clustered order of selected sequences Nucleic Alphabet a Identity Output line length a 80 Compress c Off Histogram a Off Randomization e Off Tue 5 Aug 103 15:03:53-PDT AMINO-Res-length = 2 DELetion-weight = 5 LENgth-factor = 0 Matching-weight = 1 NUCLEIC-Res-length = 4 Spread-factor = 5 3. US-09-303-040-5 o c | |o IntelliGenetics o c Solution Parameters: Histogram Randomization JS-09-303-JS-09-303-JS-09-303-JS-09-303-JS-09-303consensus 13-09-303consensors JS-09-303-US-09-303-Consensus consensus

GGATAAGCTGGTTCTGTATGAGATATTCAGAGGCAAAGAGAACCCTCAAAATGTTCATCTC

306 AAATATAAGGGCCGTACAAGCTTTGACAAGGACAACTGGACCCTGAGACCTGAGACTCCACAAGTGTTC **AAATATAAGGGCCGTACAAGCTTTGACAAGGACAACTGGACCCTGAGACTCCACAATGTTC** 

306 AAATATAAGGGCCGTACAAGCT

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245 GGATAAGCTGGTTCTGTATGAGATATTCAGAGGCAAAGAGAACCCTCAAAATGTTCATCTC

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**AGATCAAGGACAAGGGCACATATCACTGTTTCATTATAAAGGGCCCAAAGGACTAGT** ACAGTAACTTCTAATAGAACAGAAAATTCTGGCATCATAAATTTGACCTGCTCATCTATAC aaggitacccagaacctaaggagatgtattttcagctaaacactgagaatttcaactactaa **GTATGATACTGTCATGAAAAATCTCAAAATAATGTGACAGAACTGTACAACGTTTCTATC** AGCTTGCCTTTTTCAGTCCCTGAAGCACACAATGTGAGCGTCTTTTGTGCCCTGAAACTGG GOGATGOTGTCCTTTAAAACACTAAGGAAAAGGAAGAAGAAGCAGCCTGGCCCCCTCTCATG CCACGTACCTGAAGATCTGATGAAGCCCAGTGTTAAACATTTTGAAGACAGCCTCAGG agacactogagatgctcctccctacctttcatatagatgcacaacctaaggataaag 916 AATOTGAAACCATCAAAAGGGAGAGAAAAGAGAGCAAACAGACCAACGAAAGAGTACCA 489 489 611 611 733 733 794 855 911 US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-U3-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303-US-09-303consensus consensus consensus consensus US-09-303consensus consensus consensus consensus US-09-303consensus consenens

US-09-303- 977 CCACGTACCTGAGAGATCTGATGAAGCCCAGTGTGATTAACATTTTGAAGACGCCTCAGGG CCACGIACCTGAGAGATCTGATGAAGCCCAGTGATAACATTTTGAAGACAGCCTCAGGG consensus

US-09-303- 1038 GACAANATCACTAGGAAAATGGTGGCTTGGCGTGGTGACAAT US-09-303- 1038 GACAAAATCAGTAGGAAAATGGTGGCATGGCGTGCTGACAAT

GACAAAAATCAGTAGGAAAATGGTGGCTTGGCGTGCTGAAA consensus

Alignment score = 1080.00

Scoring matrix:

0

0.00

1080 1080 1080

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o | O IntelliGenetics

Similarity matrix Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group

Scores: Times: Sequence Name

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